

(c) the third segment having the amino acid sequence of a third portion of a naturally occurring protein of a pathogenic agent, the third segment being at least eleven amino acids in length and comprising two epitopes different from the epitopes of (a) and (b), provided that either

- 91
- (i) the first, second and third portions are non-contiguous portions of the same naturally occurring protein, and the sum of all three portions constitutes less than 70% of the sequence of the naturally occurring protein; or
 - (ii) the first, second and third portions are portions of three different naturally occurring proteins of one or more pathogenic agents.
-

5. (Amended) The nucleic acid of claim 1, further comprising

92 (d) a fourth segment which has the amino acid sequence of a fourth portion of a naturally occurring protein of a pathogenic agent, the fourth segment being at least eleven amino acids in length and comprising two epitopes different from the epitopes of (a), (b) and (c).

47. (Amended) A DNA encoding a hybrid polypeptide the sequence of which comprises at least one of the following segments of HPV strain 16 E6:

93 AMFQDPQERPRKLPQLCTEL (SEQ ID NO:64),
LLRREVYDFAFRDLCIVYRDGNPY (SEQ ID NO:65), and
KISEYRHYCYSLYGTTLEQQYNK (SEQ ID NO:66);

at least one of the following segments of HPV strain 16 E7:

TLHEYMLDLQPETTDLYSY (SEQ ID NO:67),
QAEPDRAHYNIVTF (SEQ ID NO:68), and
LLMGTLGIVCPICSQKP (SEQ ID NO:69);

at least one of the following segments of HPV strain 18 E6:

RRPYKLPLDCTELNTSLQDIEITCVYCKTVLELTEVFEFAFK (SEQ ID NO:152),

and

SVYGDTLEKLTNTGLYNLLIRCLRCQK (SEQ ID NO:153),

and at least one of the following segments of HPV strain 18 E7:

KATLQDIVLHLEPQNEIPV (SEQ ID NO:154),

13 HTMLCMCCKCEARI (SEQ ID NO:155), and
AFQQLFLNTLSFVCPWC (SEQ ID NO:156),

provided that the hybrid polypeptide does not comprise a sequence identical to the sequence of either full length, intact E6 or full length, intact E7 protein from HPV strain 16 or 18.

52. (Amended) A DNA encoding a hybrid polypeptide the sequence of which comprises a signal sequence and at least one of the following segments of HPV E6 and E7 proteins:

94

AMFQDPQERPRKLPQLCTEL (SEQ ID NO:64),
LLRREVYDFAFRDLCIVYRDGNPY (SEQ ID NO:65),
KISEYRHYCYSLYGTTLEQQYNK (SEQ ID NO:66),
TLHEYMLDLQPETTDLYSY (SEQ ID NO:67),
QAEPDRAHYNIVTF (SEQ ID NO:68),
RRPYKLPLDCTELNTSLQDIEITCVYCKTVLELTEVFEFAFK (SEQ ID NO:152),
SVYGDTLEKLTNTGLYNLLIRCLRCQK (SEQ ID NO:153),
KATLQDIVLHLEPQNEIPV (SEQ ID NO:154),
HTMLCMCCKCEARI (SEQ ID NO:155), and
AFQQLFLNTLSFVCPWC (SEQ ID NO:156);

provided that the hybrid polypeptide does not comprise a sequence identical to the sequence of either full length, intact E6 or full length, intact E7 protein from HPV strain 16 or 18.
